SEQUENCE LISTING

<110> Susan M. Freier
      Kenneth W. Dobie

<120> ANTISENSE MODULATION OF PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 4, P150 EXPRESSION

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ctaaagacca cagaggtgct tgccatt atg gga aat cag ctt gct ggc att gct 594
                              Met Gly Asn Gln Leu Ala Gly Ile Ala
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ccc tcc cag atc ctt tct gta gag agt tat ttt tca gat att cat gac   642
Pro Ser Gln Ile Leu Ser Val Glu Ser Tyr Phe Ser Asp Ile His Asp
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ttt gaa tat gat aaa agc ctg ggg agt act cgg ttt ttt aaa gtt gct   690
Phe Glu Tyr Asp Lys Ser Leu Gly Ser Thr Arg Phe Phe Lys Val Ala
                30   35   40

cga gcc aag cac cga gaa ggc ctg gtc gtt gtg aag gtt ttt gca att   738
Arg Ala Lys His Arg Glu Gly Leu Val Val Val Lys Val Phe Ala Ile
            45   50   55

cag gat ccc aca ttg cct tta acc agc tat aaa caa gag ctg gag gaa   786
Gln Asp Pro Thr Leu Pro Leu Thr Ser Tyr Lys Gln Glu Leu Glu Glu
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ctg aaa atc agg ctt aat tct gca cag aat tgt cta cct ttc cag aaa   834
Leu Lys Ile Arg Leu Asn Ser Ala Gln Asn Cys Leu Pro Phe Gln Lys
        75   80   85

gca tca gaa aaa gca tct gag aaa gca gct atg ctc ttt agg cag tat   882
Ala Ser Glu Lys Ala Ser Glu Lys Ala Ala Met Leu Phe Arg Gln Tyr
 90   95   100   105

gtg cga gac aat ctc tat gat cgc atc agt acc cgt cca ttc ttg aat   930
Val Arg Asp Asn Leu Tyr Asp Arg Ile Ser Thr Arg Pro Phe Leu Asn
                110   115   120

aac att gag aag cgc tgg att gct ttc cag atc ctg aca gct gtg gac   978
Asn Ile Glu Lys Arg Trp Ile Ala Phe Gln Ile Leu Thr Ala Val Asp
            125   130   135

caa gca cac aaa tct gga gtt cgt cat ggg gac atc aag act gag aat   1026
Gln Ala His Lys Ser Gly Val Arg His Gly Asp Ile Lys Thr Glu Asn
            140   145   150

gtg atg gtc acc agt tgg aat tgg gtt ctt cta act gat ttt gcc agt   1074
Val Met Val Thr Ser Trp Asn Trp Val Leu Leu Thr Asp Phe Ala Ser
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ttt aag ccc act tat ctt cca gaa gac aac ccg gca gat ttc aat tat   1122
Phe Lys Pro Thr Tyr Leu Pro Glu Asp Asn Pro Ala Asp Phe Asn Tyr
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Phe Val Asp Gly Gly Met Phe Ala Thr Glu Leu Glu Tyr Met Arg Asp
            205                 210                 215

cct tca act ccg ctt gta gac tta aat agc aat cag aga aca aga gga    1266
Pro Ser Thr Pro Leu Val Asp Leu Asn Ser Asn Gln Arg Thr Arg Gly
            220                 225                 230

gag ttg aag aga gca atg gac atc ttt tca gca ggt tgt gtg ata gct    1314
Glu Leu Lys Arg Ala Met Asp Ile Phe Ser Ala Gly Cys Val Ile Ala
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gag ctt ttt aca gaa ggt gta cca tta ttt gat ctc tct caa ctt ttg    1362
Glu Leu Phe Thr Glu Gly Val Pro Leu Phe Asp Leu Ser Gln Leu Leu
250                 255                 260                 265

gct tat aga aat gga cat ttt ttc cct gaa caa gtg cta aat aaa att    1410
Ala Tyr Arg Asn Gly His Phe Phe Pro Glu Gln Val Leu Asn Lys Ile
            270                 275                 280

gaa gat cac agt atc aga gaa ttg gta act cag atg att cac cgt gag    1458
Glu Asp His Ser Ile Arg Glu Leu Val Thr Gln Met Ile His Arg Glu
            285                 290                 295

cca gat aaa cgt tta gag gca gaa gat tac tta aaa cag cag cgt ggc    1506
Pro Asp Lys Arg Leu Glu Ala Glu Asp Tyr Leu Lys Gln Gln Arg Gly
            300                 305                 310

aat gcc ttt cct gaa ata ttt tac act ttt ctt cag ccc tac atg gcc    1554
Asn Ala Phe Pro Glu Ile Phe Tyr Thr Phe Leu Gln Pro Tyr Met Ala
            315                 320                 325

cag ttt gcc aag gaa acg ttt ctt tct gca gat gag cgt att ctg gtt    1602
Gln Phe Ala Lys Glu Thr Phe Leu Ser Ala Asp Glu Arg Ile Leu Val
330                 335                 340                 345

ata cgg aag gat ttg ggc aac att att cac aat ctc tgt gga cat gat    1650
Ile Arg Lys Asp Leu Gly Asn Ile Ile His Asn Leu Cys Gly His Asp
            350                 355                 360

ctg cca gaa aaa gcc gaa gga gag cct aag gaa aat ggg ctg gtt atc    1698
Leu Pro Glu Lys Ala Glu Gly Glu Pro Lys Glu Asn Gly Leu Val Ile
            365                 370                 375

ttg gta tct gtt ata aca tcc tgc cta cag acc ctt aaa tac tgt gat    1746
Leu Val Ser Val Ile Thr Ser Cys Leu Gln Thr Leu Lys Tyr Cys Asp
            380                 385                 390

tcc aaa cta gct gct ttg gaa ctg att ctt cat ttg gct cca aga tta    1794
Ser Lys Leu Ala Ala Leu Glu Leu Ile Leu His Leu Ala Pro Arg Leu
            395                 400                 405

agt gtt gaa atc ctt ttg gat cgt att act cca tat ctt ttg cat ttc    1842
Ser Val Glu Ile Leu Leu Asp Arg Ile Thr Pro Tyr Leu Leu His Phe
410                 415                 420                 425
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agc aat gac tct gtt cct agg gtg agg gct gaa gcc ttg agg acg ttg    1890
Ser Asn Asp Ser Val Pro Arg Val Arg Ala Glu Ala Leu Arg Thr Leu
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acc aaa gtt ctt gct ctc gtc aaa gag gtt cct cgt aat gat atc aat    1938
Thr Lys Val Leu Ala Leu Val Lys Glu Val Pro Arg Asn Asp Ile Asn
            445             450             455

att tat ccg gaa tac att ctg cca ggc ata gcc cac tta gcc caa gat    1986
Ile Tyr Pro Glu Tyr Ile Leu Pro Gly Ile Ala His Leu Ala Gln Asp
            460             465             470

gat gct act atc gtt aga cta gcc tat gct gaa aac ata gct ctg ctg    2034
Asp Ala Thr Ile Val Arg Leu Ala Tyr Ala Glu Asn Ile Ala Leu Leu
            475             480             485

gca gaa aca gct ctg aga ttc ctg gaa tta gta cag tta aaa aat ctt    2082
Ala Glu Thr Ala Leu Arg Phe Leu Glu Leu Val Gln Leu Lys Asn Leu
490             495             500             505

aat atg gaa aat gac ccc aat aat gaa gaa ata gat gag gtt aca cat    2130
Asn Met Glu Asn Asp Pro Asn Asn Glu Glu Ile Asp Glu Val Thr His
            510             515             520

cca aat gga aat tat gac aca gag ctc caa gcc tta cat gaa atg gtc    2178
Pro Asn Gly Asn Tyr Asp Thr Glu Leu Gln Ala Leu His Glu Met Val
            525             530             535

cag cag aaa gtt gtt act ttg cta agt gac cct gaa aat att gta aaa    2226
Gln Gln Lys Val Val Thr Leu Leu Ser Asp Pro Glu Asn Ile Val Lys
            540             545             550

caa acc ttg atg gaa aat gga ata aca cgg ctg tgt gta ttc ttt gga    2274
Gln Thr Leu Met Glu Asn Gly Ile Thr Arg Leu Cys Val Phe Phe Gly
555             560             565

cgt cag aaa gcc aac gat gtt ttg ttg tcc cac atg att act ttc cta    2322
Arg Gln Lys Ala Asn Asp Val Leu Leu Ser His Met Ile Thr Phe Leu
570             575             580             585

aat gat aag aat gat tgg cat cta cgt gga gca ttt ttt gat agt ata    2370
Asn Asp Lys Asn Asp Trp His Leu Arg Gly Ala Phe Phe Asp Ser Ile
            590             595             600

gtt ggt gtt gct gcc tat gtt ggc tgg caa agc tcc tca att ctc aag    2418
Val Gly Val Ala Ala Tyr Val Gly Trp Gln Ser Ser Ser Ile Leu Lys
            605             610             615

cct ctg ctg caa caa ggt ctt agt gat gct gag gaa ttt gtc att gtg    2466
Pro Leu Leu Gln Gln Gly Leu Ser Asp Ala Glu Glu Phe Val Ile Val
            620             625             630

aaa gct ctt tat gcc ctt act tgt atg tgc cag tta gga ctg cta caa    2514
Lys Ala Leu Tyr Ala Leu Thr Cys Met Cys Gln Leu Gly Leu Leu Gln
635             640             645

aaa ccc cat gtt tac gaa ttt gcc agt gat att gcc ccc ttc ctg tgt    2562
Lys Pro His Val Tyr Glu Phe Ala Ser Asp Ile Ala Pro Phe Leu Cys
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cat ccc aat tta tgg ata cgt tat ggt gcc gtg gga ttt atc aca gtg    2610
His Pro Asn Leu Trp Ile Arg Tyr Gly Ala Val Gly Phe Ile Thr Val
            670             675             680

gta gct cgt caa ata agt aca gct gat gtc tac tgt aaa ctg atg cct    2658
Val Ala Arg Gln Ile Ser Thr Ala Asp Val Tyr Cys Lys Leu Met Pro
            685             690             695

tat ctt gac cca tat att acc caa cca ata ata cag att gaa aga aaa    2706
Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu Arg Lys
            700             705             710

ctt gtt ctg ctc agt gtt tta aag gaa cca gta agt cgt tct ata ttt    2754
Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser Ile Phe
            715             720             725

gat tat gct ttg agg tct aaa gat att act agc ttg ttc aga cat ctt    2802
Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg His Leu
730             735             740             745

cac atg cgt cag aag aaa cga aat ggt tct ctt ccc gac tgc cct ccg    2850
His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys Pro Pro
            750             755             760

cca gag gat cct gcc ata gca cag ctt ctg aag aag ttg ctc tca cag    2898
Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu Ser Gln
            765             770             775

gga atg aca gag gaa gag gaa gac aaa ctt ctg gca ctg aaa gac ttc    2946
Gly Met Thr Glu Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys Asp Phe
            780             785             790

atg atg aaa tct aat aaa gca aag gcc aat ata gtg gac cag agc cat    2994
Met Met Lys Ser Asn Lys Ala Lys Ala Asn Ile Val Asp Gln Ser His
            795             800             805

ctt cat gat agt agt cag aaa ggt gta att gac ttg gca gct tta ggc    3042
Leu His Asp Ser Ser Gln Lys Gly Val Ile Asp Leu Ala Ala Leu Gly
810             815             820             825

ata act ggg aga caa gtt gat ctt gtt aaa acc aaa caa gaa cca gat    3090
Ile Thr Gly Arg Gln Val Asp Leu Val Lys Thr Lys Gln Glu Pro Asp
            830             835             840

gac aaa cgg gcc aga aaa cat gta aaa caa gac tca aat gta aat gaa    3138
Asp Lys Arg Ala Arg Lys His Val Lys Gln Asp Ser Asn Val Asn Glu
            845             850             855

gaa tgg aaa agc atg ttt ggg tca ctg gac cca cca aac atg cca cag    3186
Glu Trp Lys Ser Met Phe Gly Ser Leu Asp Pro Pro Asn Met Pro Gln
            860             865             870

gcc cta cct aaa ggg agt gat cag gag gtg att cag act ggg aaa cct    3234
Ala Leu Pro Lys Gly Ser Asp Gln Glu Val Ile Gln Thr Gly Lys Pro
875             880             885

cct cgt tcc gag tcc tct gct ggc att tgt gtc cct ttg tca act tct    3282
Pro Arg Ser Glu Ser Ser Ala Gly Ile Cys Val Pro Leu Ser Thr Ser
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Ser Gln Val Pro Glu Val Thr Thr Val Gln Asn Lys Lys Pro Val Ile
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ccg gtt tta agt agt aca atc tta cca tcc acc tat cag att cga att    3378
Pro Val Leu Ser Ser Thr Ile Leu Pro Ser Thr Tyr Gln Ile Arg Ile
            925             930                 935

aca act tgt aaa act gaa ctt cag caa ctc atc cag caa aag cgg gag    3426
Thr Thr Cys Lys Thr Glu Leu Gln Gln Leu Ile Gln Gln Lys Arg Glu
            940             945                 950

cag tgc aat gct gag aga ata gct aag cag atg atg gaa aat gct gaa    3474
Gln Cys Asn Ala Glu Arg Ile Ala Lys Gln Met Met Glu Asn Ala Glu
        955             960             965

tgg gag agt aaa cca cca cca cct gga tgg cgt cct aaa ggg ctg tta    3522
Trp Glu Ser Lys Pro Pro Pro Pro Gly Trp Arg Pro Lys Gly Leu Leu
970             975             980                 985

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Val Ala His Leu His Glu His Lys Ser Ala Val Asn Arg Ile Arg Val
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Ser Asp Glu His Ser Leu Phe Ala Thr Cys Ser Asn Asp Gly Thr Val
                1005            1010            1015

aaa atc tgg aac agt caa aag atg gag ggg aag acc acc act acc aga    3666
Lys Ile Trp Asn Ser Gln Lys Met Glu Gly Lys Thr Thr Thr Thr Arg
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tct att ctt aca tac agc cga att gga gga cga gtc aag acg ctc aca    3714
Ser Ile Leu Thr Tyr Ser Arg Ile Gly Gly Arg Val Lys Thr Leu Thr
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ttc tgc caa ggc tcc cac tat tta gcc ata gca tct gat aat ggt gct    3762
Phe Cys Gln Gly Ser His Tyr Leu Ala Ile Ala Ser Asp Asn Gly Ala
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gtc cag ctt ctt gga att gag gct tct aag ctg ccc aag tct cct aaa    3810
Val Gln Leu Leu Gly Ile Glu Ala Ser Lys Leu Pro Lys Ser Pro Lys
                1070            1075            1080

atc cat cct cta caa agc aga att cta gat cag aag gag gac ggt tgt    3858
Ile His Pro Leu Gln Ser Arg Ile Leu Asp Gln Lys Glu Asp Gly Cys
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gtt gtg gat atg cat cac ttc aac tct gga gca cag tct gtt ctt gcc    3906
Val Val Asp Met His His Phe Asn Ser Gly Ala Gln Ser Val Leu Ala
            1100            1105            1110

tat gcc act gtg aat ggc tct ctg gtt ggc tgg gac ctt agg tct tca    3954
Tyr Ala Thr Val Asn Gly Ser Leu Val Gly Trp Asp Leu Arg Ser Ser
            1115            1120            1125

agc aat gcg tgg act tta aag cat gat tta aag tcg ggc ctc atc act    4002
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1130            1135            1140                1145
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agt ggt acc atg gct tgt tgg gac atg agg ttc cag ttg cca att tca   4098
Ser Gly Thr Met Ala Cys Trp Asp Met Arg Phe Gln Leu Pro Ile Ser
            1165            1170                1175

agt cac tgt cat cct tcc agg gct cga atc aga cgc ctc tca atg cac   4146
Ser His Cys His Pro Ser Arg Ala Arg Ile Arg Arg Leu Ser Met His
            1180            1185                1190

cct ctg tat cag tcc tgg gtg att gca gct gtt cag ggc aac aac gaa   4194
Pro Leu Tyr Gln Ser Trp Val Ile Ala Ala Val Gln Gly Asn Asn Glu
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gtg tcc atg tgg gac atg gag act ggt gac aga aga ttt act ctc tgg   4242
Val Ser Met Trp Asp Met Glu Thr Gly Asp Arg Arg Phe Thr Leu Trp
1210                1215                1220                1225

gcc agc agt gca cca cca ctt tct gaa tta cag cct tct cct cat agc   4290
Ala Ser Ser Ala Pro Pro Leu Ser Glu Leu Gln Pro Ser Pro His Ser
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gtc cat ggt atc tac tgt agt cct gca gat gga aat cct atc cta cta   4338
Val His Gly Ile Tyr Cys Ser Pro Ala Asp Gly Asn Pro Ile Leu Leu
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aca gct ggc tca gat atg aaa ata agg ttt tgg gac ttg gct tac cca   4386
Thr Ala Gly Ser Asp Met Lys Ile Arg Phe Trp Asp Leu Ala Tyr Pro
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gaa agg tcc tat gtt gtt gca gga agt act agt tcc cca tct gtg tcc   4434
Glu Arg Ser Tyr Val Val Ala Gly Ser Thr Ser Ser Pro Ser Val Ser
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tac tac agg aaa ata att gaa ggc act gaa gtt gtc cag gaa att cag   4482
Tyr Tyr Arg Lys Ile Ile Glu Gly Thr Glu Val Val Gln Glu Ile Gln
1290                1295                1300                1305

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Asn Lys Gln Lys Val Gly Pro Ser Asp Asp Thr Pro Arg Arg Gly Pro
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gag tcc ctg ccc gtg gga cat cat gac atc atc act gat gtc gcc aca   4578
Glu Ser Leu Pro Val Gly His His Asp Ile Ile Thr Asp Val Ala Thr
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ttc cag acc aca cag ggc ttc atc gta act gct tct aga gat ggg att   4626
Phe Gln Thr Thr Gln Gly Phe Ile Val Thr Ala Ser Arg Asp Gly Ile
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Val Lys Val Trp Lys  *
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